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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
09/099,823	06/19/98	BILLING-MEDEL	P 0200-0023.20

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STEVEN F WEINSTOCK
ABBOTT LABORATORIES
D-377/AP6D
100 ABBOTT PARK ROAD
ABBOTT PARK IL 60064-3500

EXAMINER	
ENEWOLD, J	
ART UNIT	**PAPER NUMBER**
1655	11

DATE MAILED: 02/02/00

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

Office Action Summary	Application No.	Applicant(s)	
	09/099,823	BILLING-MEDEL ET AL.	
	Examiner	Art Unit	
	Jeanine A Enewold	1655	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136 (a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).

Status

1)☐ Responsive to communication(s) filed on *30 December 1999* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☐ Claim(s) *1-44* is/are pending in the application.

4a) Of the above claim(s) *17-29,31,32,34,36,37,43 and 44* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☐ Claim(s) *1-16,30,33,35 and 38-42* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claims _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are objected to by the Examiner.

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. § 119

13)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d).

a)☐ All b)☐ Some * c)☐ None of the CERTIFIED copies of the priority documents have been:

1.☐ received.

2.☐ received in Application No. (Series Code / Serial Number) _____ .

3.☐ received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgement is made of a claim for domestic priority under 35 U.S.C. & 119(e).

Attachment(s)

14) ☒ Notice of References Cited (PTO-892)
15) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
16) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) *3, 6* .
17) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
18) ☐ Notice of Informal Patent Application (PTO-152)
19) ☐ Other: .

DETAILED ACTION

Election/Restrictions

1. Applicant's election of Group I (Claims 1-16, 30, 33, 35, 38-42) in Paper No. 10 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

2. Claims 1-16, 30, 33, 35, 38-42 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a method for detecting the presence of a target BS124 polynucleotide comprising SEQ ID NO: 15 and the complements of SEQ ID NO: 1-5, does not reasonably provide enablement for BS124 polynucleotides having "at least 50% identity with" SEQ ID NO: 1-5 and fragments or complements thereof, or for genes encoding BS124 proteins having "at least 50% identity" with SEQ ID NO: 22. The specification does not enable any person skilled in the art to which it

pertains, or with which it is most nearly connected, to make the invention commensurate in scope with these claims.

It is well established that to claim a chemical compound, such as a polynucleotide, the inventor must be able to define the compound so as to distinguish the compound from other materials. The claimed compound must be defined in terms so as to provide a permanent and definite idea of the complete and operative invention. In the instant case, the claimed polynucleotides have not been clearly defined in terms of structure and/or function, and therefore one cannot make and use the polynucleotides as claimed. As stated in Vaek (CAFC 20 USPQ2d 1438, the "specification must teach those of skill in the art how to make and use the invention as broadly as it is claimed." However, in order to be able to make an invention, one must be able to clearly define that invention.

The claims are drawn to a method of detecting a polynucleotide having "at least 50% identity with" SEQ ID NO:s 1-5 and fragments and complements thereof (Claims 1-9), to polynucleotides having "at least 50% identity with" SEQ ID NO:s 1-5, and fragments and complements thereof, and to a gene which codes for an BS124 protein "which comprises an amino acid sequence having at least 50% identity to SEQ ID NO: 22" (Claim 38). The specification teaches a single BS124 consensus polynucleotide, SEQ ID NO: 5, the sequence of which was assembled from 3 EST clones (SEQ ID NO:1-3) and the fill-length clone (SEQ ID NO: 4) (pg. 57).

Applicant's specification discloses a single BS124 gene sequence and a single BS124 protein sequence. Yet Applicant's claims, which are to sequences having "at least 50% identity" with a few sequences taught in the specification, may encompass thousands of polynucleotides. As discussed below, Applicant's definition of "% identity" is insufficient to provide a skilled artisan with the guidance necessary to clearly define the sequences encompassed by this claim language. Without specific teachings with respect to the methods used to determine "% identity", a skilled artisan could not be expected to identify or make the polynucleotides encompassed by the instant claims. Furthermore, irrespective of how "% identity" is defined, it is clear that by any definition of "% identity", may sequences encompassed by applicant's claims, and particularly those having "at least 50% identity" with fragments of the sequences taught in the specification, would bear little resemblance to the single BS124 consensus sequence that Applicant has taught. Neither the specification nor the claims set forth any particular structural or functional characteristics that a skilled artisan could use to identify polynucleotides that constitute BS124 polynucleotides, other than those described by SEQ ID NO. The term "BS124" is not an art recognized term, and thus the prior art is silent with respect to structural and functional features that may be used to identify such polynucleotides. Furthermore, in teaching a single BS124 polynucleotide sequence and a single BS124 protein sequence, applicant clearly has not taught the isolation of a representative number of polynucleotides that fall within the scope of the large genus encompassed by the instant claims. Thus, while the teachings of the

specification and of the prior art would enable a skilled artisan to make and used polynucleotides comprising SEQ ID NO: 1-5 and the complements of SEQ ID NO: 1-5, as well as polynucleotides encoding SEQ ID NO: 22, it is unpredictable as to whether a skilled artisan could make and use BS124 polynucleotides having "at least 50% identity" with SEQ ID NO: 1-5 and fragments and complements thereof, or genes encoding BS124 proteins having "at least 50% identity" with SEQ ID NO: 22. It would require undue experimentation for a skilled artisan to make and use the invention as broadly as it is claimed.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

3. Claims 1-16, 30, 33, 35, 38-42 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

A) Claims 1-16, 33, 35, 38-42 are indefinite over the recitation "at least 50% identity" since it is unclear what is meant by 50% identity. There is no fixed, art recognized definition for the term "% identity". While the specification discusses what "identity" and "% identity" mean "in general" (pg. 15), a specific and precise definition of "% identity" that may be used to identify those sequences encompassed by applicant's

claims is not provided. For example, it is unclear if percent identity is determined for the entire nucleotide sequence or over a certain range of nucleotides. Furthermore, while the specification discloses that particular software packages may be used to calculate % identity (pg. 15), the specification does not set forth specific algorithms, including the require operator defined parameters, that are to be used to calculate "% identity". In the absence of a specific definition in the specification for "% identity" and in the absence of a recitation in the claims as to the algorithm and parameters used to determine percent identity, a skilled artisan could not determine the metes and bounds of the claimed subject matter.

B) Claims 1-16, 30, 33, 35, 40-42 are indefinite over the recitation "complements thereof". It is unclear what complements of SEQ ID NO:1-5 entails. It is unclear as to whether complements means the complementary sequence according to Watson-Crick basepairing, structural complements, or functional complements. As a result, the metes and bounds of the claims are unclear.

C) Claims 1-16, 30, 33, 35, 38-42 are indefinite over the recitation "or SEQUENCE ID NO: 5, and fragments or complements thereof". It is unclear whether applicant intended to claim only the complement of SEQ ID NO: 5 or all of the complements of SEQ ID NO:s 1-5. Further, it is unclear whether SEQ ID NO: 2 and 3 are being claimed twice in Claim 33 or whether fragments of the polynucleotides of SEQ ID NO:2 and fragments of the polynucleotides of SEQ ID NO: 3 are being claimed. Thus, the metes and bounds of the claimed invention are unclear.

D) Claims 11-14,16 are indefinite over the recitation of the phrase "derived from" in Claim 11. In the specification, applicant has defined the term "derived from" as "a polynucleotide sequences which comprises a contiguous sequence of approximately at least about 6 nucleotides....corresponding, i.e., identical or complementary to, a region of the designated nucleotide sequences" (pg. 16). Based on this definition, it is unclear as to what polynucleotides and nucleic acids would be encompassed by the language "derived from". For example, while the term "identical has a well known meaning, it is unclear as to what degree of complementarily might be encompassed by the term "complementary".

E) Claims 1-16, 30, 33, 35, 38-42 are indefinite over the recitation of the term "BS124". It is unclear what is meant by this term, and as to how applicant may intent for this term to limit the claims. BS124 is not an art recognized term, and the specification does not offer a clear definition of BS124. While applicant describes identifying "EST's corresponding to the consensus sequence of BS124" in lung tissue libraries and indicates that lung cancer may be associated with expression of BS124 (see, for example, pg. 60), applicant also describes an "BS124-specific polynucleotide" as having "at least 50% identity with a polynucleotide selected from the group consisting of SEQUENCE ID NO: 1, SEQUENCE ID NO: 2, SEQUENCE ID NO: 4, SEQUENCE NO: 5, and complements therof, and (b) fragments of SEQUENCE ID NO: 1, SEQUENCE ID NO: 2, and SEQUENCE ID NO:3 (pg. 6), and defines a "polypeptide encoded by BS124" as a polypeptide comprising "an amino acid sequence selected from the group

consisting of SEQUENCE ID NO: 21, SEQUENCE ID NO: 22, SEQUENCE ID NO: 23, SEQUENCE ID NO: 24, SEQUENCE ID NO: 25, SEQUENCE ID NO: 26, and fragments thereof" (pg. 7). As these structural descriptions of BS124 polynucleotides and polypeptides encompass thousands of sequences which may or may not be expressed in lung tissue, it is unclear as to how the term "BS124" further limits the claims.

F) Claim 11 is indefinite over the recitation "hybridizes selectively". While the meaning of the term "hybridize" is well known in the art, the phrase "hybridizes selectively" could have different meaning to different people of skill in the art. As a result, it is unclear as to what extent the phrase "wherein said polynucleotide is capable of hybridizes selectively to the nucleic acid of said BS124 gene" further limits the claims. Therefore, the metes and bounds of the claims are unclear.

G) Claims 15-16 are indefinite over the recitation of the phrase "comprising a nucleic acid sequence that includes an open reading frame derived from BS124 operably linked to a control sequence compatible with a desired host" in Claim 15. It is unclear as to whether the open reading frame is "operably linked to a control sequence..", or, alternatively, whether BS124 is "operably linked to a control sequence..". If Applicant's intent was to indicate the former, the claim could be amended to recite "comprising a nucleic acid sequence that includes an open reading frame derived from BS124, wherein said open reading frame is operably linked to a control sequence compatible with a desired host".

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless --
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

4. Claim 11 is rejected under 35 U.S.C. 102(b) as being anticipated by Hawkins (GenBank Accession No: ACOO2098, May 1997).

Hawkins teaches GenBank Accession No. ACOO2098, a human chromosome 9 clone of which a 122 base pair sequence is 99.2% identical to base pairs 5815-5694 of SEQ ID NO: 1 (See attachment)(limitations of Claims 11). Hawkins' teachings clearly encompass polynucleotides having "at least 50% identity" with sequences encompassed by the instant claims, as well as fragments and complements thereof.

5. Claim 11 is rejected under 35 U.S.C. 102(a) as being anticipated by Hawkins GenBank Accession NO: AC002320, July 1997).

Hawkins teaches GenBank Accession No. AC002320, a human chromosome 9 clone of which a 122 base pair sequence is 99.2% identical to base pairs 48493-48372

of SEQ ID NO: 1 (See attachment)(limitations of Claims 11). Hawkins' teachings clearly encompass polynucleotides having "at least 50% identity" with sequences encompassed by the instant claims, as well as fragments and complements thereof.

6. Claims 11-16, 30, 33, 35, 38-39 are rejected under 35 U.S.C. 102(a) as being anticipated by NCI (GenBank Accession No: AI1251747, 1997).

NCI teaches GenBank Accession No. AI1251747, a human cDNA, of which a 132 base pair sequence is 98.5% identical to base pairs 114-245 of SEQ ID NO: 2, a 337 base pair sequence is 99.7% identical to base pairs 1-337 of SEQ ID NO: 3, a 467 base pair sequence is 99.1% identical to base pairs 226-692 of SEQ ID NO: 4, and a 467 base pair sequence is 99.1% identical to base pairs 226-692 of SEQ ID NO: 5 (See attachment)(limitations of Claims 11 and 39). NCI's teachings clearly encompass polynucleotides having "at least 50% identity" with sequences encompassed by the instant claims, as well as fragments and complements thereof. Hillier's polynucleotides are pT7T3D clones, and therefore have been produced by methods that constitute both recombinant and synthetic techniques (Claims 12-13). As NCI's polynucleotides have been cloned into the multiple cloning site of pT7T3D, NCI's polynucleotides are "operably linked" to either the T7 or T3 promoter (Claim 15). With respect to Claims 16 and 30, NCI's clones are stored in E. coli DH10B. With respect to Claims 14 and 30, NCI's polynucleotides would be expected to encodes "at least one BS124 epitope" since the polynucleotides contain regions identical to the claimed polynucleotides. With

respect to Claim 39, NCI's polynucleotides clearly comprise DNA "having at least 50% identity" with SEQ ID NO: 4 or SEQ ID NO: 5. NCI's polynucleotide encodes a 110 amino acid sequence of the polypeptide of SEQ ID NO: 22 (limitations of Claim 38).

7. Claims 11-16, 30, 33, 35, 38-39 are rejected under 35 U.S.C. 102(b) as being anticipated by Hillier (GenBank Accession No: AA460323, September 12, 1996).

Hillier et al. (herein referred to as Hillier) teaches GenBank Accession No. AA460323, a human testis encoding cDNA, of which a 337 base pair sequence is 100% identical to base pairs 1-337 of SEQ ID NO: 3, and a 337 base pair sequence is 100% identical to nucleotides 354-690 of SEQ ID NO: 4 (See attachment)(limitations of Claims 11 and 39). Hillier's teachings clearly encompass polynucleotides having "at least 50% identity" with sequences encompassed by the instant claims, as well as fragments and complements thereof. Hillier's polynucleotides are pT7T3D clones, and therefore have been produced by methods that constitute both recombinant and synthetic techniques (Claims 12-13). As Hillier's polynucleotides have been cloned into the multiple cloning site of pT7T3D, Hillier's polynucleotides are "operably linked" to either the T7 or T3 promoter (Claim 15). With respect to Claims 16 and 30, Hillier's clones are stored in E. coli DH10B. With respect to Claims 14 and 30, Hillier's polynucleotides would be expected to encodes "at least one BS124 epitope" since the polynucleotides contain regions identical to the claimed polynucleotides. With respect to Claim 39, Hillier's polynucleotides clearly comprise DNA "having at least 50% identity" with SEQ ID NO: 4

or SEQ ID NO: 5. Hillier's polynucleotide encodes a 67 amino acid sequence of the polypeptide of SEQ ID NO: 22 (limitations of Claim 38).

8. Claims 11-16, 30, 33, 35, 38-39 are rejected under 35 U.S.C. 102(b) as being anticipated by Hillier (GenBank Accession No: AA460385, September 12, 1996).

Hillier et al. (herein referred to as Hillier) teaches GenBank Accession No. AA460385, a human testis encoding cDNA, of which a 334 base pair sequence is 100% identical to base pairs 3-337 of SEQ ID NO: 3, a 412 base pair sequence is 99.8% identical to base pairs 277-688 of SEQ ID NO: 4, and a 412 base pair sequence is 99.8% identical to nucleotides 277-688 of SEQ ID NO: 5 (See attachment)(limitations of Claims 11 and 39). Hillier's teachings clearly encompass polynucleotides having "at least 50% identity" with sequences encompassed by the instant claims, as well as fragments and complements thereof. Hillier's polynucleotides are pT7T3D clones, and therefore have been produced by methods that constitute both recombinant and synthetic techniques (Claims 12-13). As Hillier's polynucleotides have been cloned into the multiple cloning site of pT7T3D, Hillier's polynucleotides are "operably linked" to either the T7 or T3 promoter (Claim 15). With respect to Claims 16 and 30, Hillier's clones are stored in E. coli DH10B. With respect to Claims 14 and 30, Hillier's polynucleotides would be expected to encodes "at least one BS124 epitope" since the polynucleotides contain regions identical to the claimed polynucleotides. With respect to Claim 39, Hillier's polynucleotides clearly comprise DNA "having at least 50%

identity" with SEQ ID NO: 4 or SEQ ID NO: 5. Hillier's polynucleotide encodes a 91 amino acid sequence of the polypeptide of SEQ ID NO: 22 (limitations of Claim 38).

9. Claims 11-16, 30, 33, 35, 38-40 are rejected under 35 U.S.C. 102(b) as being anticipated by NCI (GenBank Accession No: AI143970, September 12, 1996).

NCI (teaches GenBank Accession No. AI143970, a human testis cDNA, of which a 332 base pair sequence is 99.4% identical to base pairs 1-332 of SEQ ID NO: 3, and a 334 base pair sequence is 99.1% identical to base pairs 359-692 of SEQ ID NO: 4 (See attachment)(limitations of Claims 11 and 39). NCI's teachings clearly encompass polynucleotides having "at least 50% identity" with sequences encompassed by the instant claims, as well as fragments and complements thereof. Hillier's polynucleotides are pT7T3D clones, and therefore have been produced by methods that constitute both recombinant and synthetic techniques (Claims 12-13). As NCI's polynucleotides have been cloned into the multiple cloning site of pT7T3D, NCI's polynucleotides are "operably linked" to either the T7 or T3 promoter (Claim 15). With respect to Claims 16 and 30, NCI's clones are stored in E. coli DH10B. With respect to Claims 14 and 30, NCI's polynucleotides would be expected to encodes "at least one BS124 epitope" since the polynucleotides contain regions identical to the claimed polynucleotides. With respect to Claim 39, NCI's polynucleotides clearly comprise DNA "having at least 50% identity" with SEQ ID NO: 4 or SEQ ID NO: 5. NCI's polynucleotide encodes a 65 amino acid sequence of the polypeptide of SEQ ID NO: 22 (limitations of Claim 38).

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

10. Claims 1-9 are rejected under 35 U.S.C. 103(a) as being unpatentable over Nangaku et al (Immunogenetics, 1997) in view of Hawkins (GenBank Accession No: ACOO2098, May 1997) or Hawkins (GenBank Accession NO: AC002320, July 1997) or NCI (GenBank Accession No: AI1251747, 1997) or Hillier (GenBank Accession No: AA460323, September 12, 1996) or Hillier (GenBank Accession No: AA460385, September 12, 1996) or NCI (GenBank Accession No: AI143970, September 12, 1996).

Nangaku teaches the identification of a new human gene from the EST database. "The EST database is a new tool that can be used to find new human genes and many partial sequences of new human genes have been discovered using this database" (pg. 101, col. 2). The identification method taught by Nangaku includes the identification of the EST sequences, followed by Northern blot using the EST sequence as a probe, isolation of cDNA clone, and DNA sequencing. The Northern blot method includes separation of RNA on an agarose gel and transferring to nitrocellulose filter

prior to hybridizing with a probe labeled with a label (limitations of Claim 2). The filter was hybridized with a labeled probe (pg. 100, col. 1, para 1).

Nangaku does not specifically teach a method of detecting a BS124 polynucleotide.

However, Hawkins teaches GenBank Accession No. ACOO2098, a human chromosome 9 clone of which a 122 base pair sequence is 99.2% identical to base pairs 5815-5694 of SEQ ID NO: 1 (See attachment)(limitations of Claims 11). Hillier's teachings clearly encompass polynucleotides having "at least 50% identity" with sequences encompassed by the instant claims, as well as fragments and complements thereof.

Hawkins teaches GenBank Accession No. AC002320, a human chromosome 9 clone of which a 122 base pair sequence is 992% identical to base pairs 48493-48372 of SEQ ID NO: 1 (See attachment)(limitations of Claims 11). Hillier's teachings clearly encompass polynucleotides having "at least 50% identity" with sequences encompassed by the instant claims, as well as fragments and complements thereof.

NCI (teaches GenBank Accession No. AI1251747, a human cDNA, of which a 132 base pair sequence is 98.5% identical to base pairs 114-245 of SEQ ID NO: 2, a 337 base pair sequence is 99.7% identical to base pairs 1-337 of SEQ ID NO: 3, a 467 base pair sequence is 99.1% identical to base pairs 226-692 of SEQ ID NO: 4, and a 467 base pair sequence is 99.1% identical to base pairs 226-692 of SEQ ID NO: 5 (See attachment)(limitations of Claims 11 and 39). NCI's teachings clearly encompass

polynucleotides having "at least 50% identity" with sequences encompassed by the instant claims, as well as fragments and complements thereof. Hillier's polynucleotides are pT7T3D clones, and therefore have been produced by methods that constitute both recombinant and synthetic techniques (Claims 12-13). As NCI's polynucleotides have been cloned into the multiple cloning site of pT7T3D, NCI's polynucleotides are "operably linked" to either the T7 or T3 promoter (Claim 15). With respect to Claims 16 and 30, NCI's clones are stored in E. coli DH10B. With respect to Claims 14 and 30, NCI's polynucleotides would be expected to encodes "at least one BS124 epitope" since the polynucleotides contain regions identical to the claimed polynucleotides. With respect to Claim 39, NCI's polynucleotides clearly comprise DNA "having at least 50% identity" with SEQ ID NO: 4 or SEQ ID NO: 5. NCI's polynucleotide encodes a 110 amino acid sequence of the polypeptide of SEQ ID NO: 22 (limitations of Claim 38).

Hillier et al. (herein referred to as Hillier) teaches GenBank Accession No. AA460323, a human testis encoding cDNA, of which a 337 base pair sequence is 100% identical to base pairs 1-337 of SEQ ID NO: 3, and a 337 base pair sequence is 100% identical to nucleotides 354-690 of SEQ ID NO: 4 (See attachment)(limitations of Claims 11 and 39). Hillier's teachings clearly encompass polynucleotides having "at least 50% identity" with sequences encompassed by the instant claims, as well as fragments and complements thereof. Hillier's polynucleotides are pT7T3D clones, and therefore have been produced by methods that constitute both recombinant and synthetic techniques (Claims 12-13). As Hillier's polynucleotides have been cloned into the multiple cloning

site of pT7T3D, Hillier's polynucleotides are "operably linked" to either the T7 or T3 promoter (Claim 15). With respect to Claims 16 and 30, Hillier's clones are stored in E. coli DH10B. With respect to Claims 14 and 30, Hillier's polynucleotides would be expected to encodes "at least one BS124 epitope" since the polynucleotides contain regions identical to the claimed polynucleotides. With respect to Claim 39, Hillier's polynucleotides clearly comprise DNA "having at least 50% identity" with SEQ ID NO: 4 or SEQ ID NO: 5. Hillier's polynucleotide encodes a 67 amino acid sequence of the polypeptide of SEQ ID NO: 22 (limitations of Claim 38).

Hillier et al. (herein referred to as Hillier) teaches GenBank Accession No. AA460385, a human testis encoding cDNA, of which a 334 base pair sequence is 100% identical to base pairs 3-337 of SEQ ID NO: 3, a 412 base pair sequence is 99.8% identical to base pairs 277-688 of SEQ ID NO: 4, and a 412 base pair sequence is 99.8% identical to nucleotides 277-688 of SEQ ID NO: 5 (See attachment)(limitations of Claims 11 and 39). Hillier's teachings clearly encompass polynucleotides having "at least 50% identity" with sequences encompassed by the instant claims, as well as fragments and complements thereof. Hillier's polynucleotides are pT7T3D clones, and therefore have been produced by methods that constitute both recombinant and synthetic techniques (Claims 12-13). As Hillier's polynucleotides have been cloned into the multiple cloning site of pT7T3D, Hillier's polynucleotides are "operably linked" to either the T7 or T3 promoter (Claim 15). With respect to Claims 16 and 30, Hillier's clones are stored in E. coli DH10B. With respect to Claims 14 and 30, Hillier's

polynucleotides would be expected to encodes "at least one BS124 epitope" since the polynucleotides contain regions identical to the claimed polynucleotides. With respect to Claim 39, Hillier's polynucleotides clearly comprise DNA "having at least 50% identity" with SEQ ID NO: 4 or SEQ ID NO: 5. Hillier's polynucleotide encodes a 91 amino acid sequence of the polypeptide of SEQ ID NO: 22 (limitations of Claim 38).

NCI (teaches GenBank Accession No. AI143970, a human testis cDNA, of which a 332 base pair sequence is 99.4% identical to base pairs 1-332 of SEQ ID NO: 3, and a 334 base pair sequence is 99.1% identical to base pairs 359-692 of SEQ ID NO: 4 (See attachment)(limitations of Claims 11 and 39). NCI's teachings clearly encompass polynucleotides having "at least 50% identity" with sequences encompassed by the instant claims, as well as fragments and complements thereof. Hillier's polynucleotides are pT7T3D clones, and therefore have been produced by methods that constitute both recombinant and synthetic techniques (Claims 12-13). As NCI's polynucleotides have been cloned into the multiple cloning site of pT7T3D, NCI's polynucleotides are "operably linked" to either the T7 or T3 promoter (Claim 15). With respect to Claims 16 and 30, NCI's clones are stored in E. coli DH10B. With respect to Claims 14 and 30, NCI's polynucleotides would be expected to encodes "at least one BS124 epitope" since the polynucleotides contain regions identical to the claimed polynucleotides. With respect to Claim 39, NCI's polynucleotides clearly comprise DNA "having at least 50% identity" with SEQ ID NO: 4 or SEQ ID NO: 5. NCI's polynucleotide encodes a 65 amino acid sequence of the polypeptide of SEQ ID NO: 22 (limitations of Claim 38).

Therefore, it would have been **prima facie** obvious to one of ordinary skill in the art at the time the claimed invention was made to have modified the method of Nangaku with the teaching of Hawkins (GenBank Accession No: ACOO2098, May 1997) or Hawkins (GenBank Accession NO: AC002320, July 1997) or NCI (GenBank Accession No: AI1251747, 1997) or Hillier (GenBank Accession No: AA460323, September 12, 1996) or Hillier (GenBank Accession No: AA460385, September 12, 1996) or NCI (GenBank Accession No: AI143970, September 12, 1996) to obtain the claimed invention because the skilled artisan would have been motivated to have used the ESTs taught by the cited references to have identified the corresponding full nucleotide coding sequence because Nangaku et al specifically taught that ESTs were very effective for this objective. The ordinary artisan would also have been motivated to have used the cDNA sequences obtained in Nangaku using the ESTs of Hawkins, NCI, and Hillier to locate the corresponding gene on its chromosome.

11. Claims 10 and 35 are rejected under 35 U.S.C. 103(a) as being unpatentable over Nangaku et al (Immunogenetics, 1997) in view of Hawkins (GenBank Accession No: ACOO2098, May 1997) or Hawkins GenBank Accession NO: AC002320, July 1997) or NCI (GenBank Accession No: AI1251747, 1997) or Hillier (GenBank Accession No: AA460323, September 12, 1996) or Hillier (GenBank Accession No: AA460385, September 12, 1996) or NCI (GenBank Accession No: AI143970, September 12, 1996) as applied to Claims 1-9 above, further in view of Cohen (US. Pat. 5,939,265).

Neither Nangaku et al (Immunogenetics, 1997) nor Hawkins (GenBank Accession No: ACOO2098, May 1997) or Hawkins GenBank Accession NO: AC002320, July 1997) or NCI (GenBank Accession No: AI1251747, 1997) or Hillier (GenBank Accession No: AA460323, September 12, 1996) or Hillier (GenBank Accession No: AA460385, September 12, 1996) or NCI (GenBank Accession No: AI143970, September 12, 1996) specifically teaches packaging the EST probes as a test kit.

However, Cohen teaches a test kit which contains polynucleotide fragments employed for an assay. Further this test kit can be provided to contain not only the polynucleotides but also containers with tools useful for collecting test samples (col. 5, lines 23-40).

Therefore, it would have been **prima facie** obvious to one of ordinary skill in the art at the time the invention was made to have packaged polynucleotides of Hawkins (GenBank Accession No: ACOO2098, May 1997) or Hawkins GenBank Accession NO: AC002320, July 1997) or NCI (GenBank Accession No: AI1251747, 1997) or Hillier (GenBank Accession No: AA460323, September 12, 1996) or Hillier (GenBank Accession No: AA460385, September 12, 1996) or NCI (GenBank Accession No: AI143970, September 12, 1996) for use in the method of Nangaku in a kit as taught by Cohen for the expected benefits of convenience and cost-effectiveness of performing the method of Nangaku with Hawkins (GenBank Accession No: ACOO2098, May 1997) or Hawkins GenBank Accession NO: AC002320, July 1997) or NCI (GenBank Accession No: AI1251747, 1997) or Hillier (GenBank Accession No: AA460323,

September 12, 1996) or Hillier (GenBank Accession No: AA460385, September 12, 1996) or NCI (GenBank Accession No: AI143970, September 12, 1996).

Conclusion

12. No claims allowable.

13. Any inquiry concerning this communication or earlier communications from the examiner should be directed to examiner Jeanine Enewold whose telephone number is (703) 306-5817. The examiner can normally be reached Monday-Thursday from 7:00 AM to 4:30 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Jones, can be reached on (703) 308-1152. The fax number for this Group is (703) 305- 3014.

Any inquiry of a general nature should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Jeanine Enewold
January 27, 2000

LISA B. ARTHUR
PRIMARY EXAMINER
GROUP 1800 1600